

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 09:57:30 ; Search time 7349 Seconds

(without alignment)
11402.551 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataaagtaag.....ctcttccttcagtgcaag 1772

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1772 | 100.0 | 1772 | 6 | AX063520 Sequence |
| 2 | 1772 | 100.0 | 1803 | 6 | AX063522 Sequence |
| 3 | 1729.8 | 97.6 | 168173 | 8 | AP004988 Oryza sat |
| 4 | 1686 | 95.1 | 1686 | 6 | AX063525 Sequence |
| 5 | 1082.4 | 61.1 | 2000 | 6 | AX656635 Sequence |
| 6 | 103.8 | 5.9 | 139653 | 2 | AP005890 Oryza sat |
| 7 | 103.8 | 5.9 | 161865 | 8 | AP005912 Oryza sat |
| 8 | 99.8 | 5.6 | 173770 | 8 | OSJN00076 |
| 9 | 99.2 | 5.6 | 88044 | 8 | AL606637 Oryza sat |
| 10 | 99 | 5.6 | 159636 | 8 | AC090485 |
| 11 | 98.8 | 5.6 | 121202 | 8 | AC090485 Genomic S |
| 12 | 98.8 | 5.6 | 135914 | 8 | AP004190 Oryza sat |
| 13 | 98.2 | 5.5 | 134058 | 8 | AP003883 Oryza sat |
| 14 | 98.2 | 5.5 | 300029 | 8 | AC037425 Oryza sat |
| 15 | 97.4 | 5.5 | 2000 | 6 | AE017105 Oryza sat |
| 16 | 97.4 | 5.5 | 126040 | 8 | AX656799 Sequence |
| 17 | 97.2 | 5.5 | 148220 | 8 | AC135495 Oryza sat |
| 18 | 96.8 | 5.5 | 170759 | 8 | AC120533 Oryza sat |
| 19 | 96 | 5.4 | 142772 | 8 | AP003271 Oryza sat |
| | | | | | AP004184 Oryza sat |

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| C 20 | 96 | 5.4 | 143046 | 8 | AP004191 | AP004191 Oryza sat |
| 21 | 95.8 | 5.4 | 103297 | 8 | AP005288 | AP005288 Oryza sat |
| 22 | 95.8 | 5.4 | 116351 | 8 | AP005574 | AP005574 Oryza sat |
| C 23 | 95.8 | 5.4 | 140823 | 8 | AP005866 | AP005866 Oryza sat |
| C 24 | 95.8 | 5.4 | 141582 | 8 | AC092076 | AC092076 Oryza sat |
| C 25 | 95.8 | 5.4 | 144190 | 2 | AP004112 | AP004112 Oryza sat |
| 26 | 95.8 | 5.4 | 144252 | 8 | AP005399 | AP005399 Oryza sat |
| C 27 | 95.8 | 5.4 | 146551 | 8 | AP004621 | AP004621 Oryza sat |
| 28 | 95.8 | 5.4 | 154192 | 8 | AP004272 | AP004272 Oryza sat |
| C 29 | 95 | 5.4 | 103234 | 2 | AP003997 | AP003997 Oryza sat |
| C 30 | 95 | 5.4 | 157248 | 8 | AP004300 | AP004300 Oryza sat |
| C 31 | 94.4 | 5.3 | 128795 | 8 | CNS08CB1 | AL844878 Oryza sat |
| C 32 | 94.4 | 5.3 | 150703 | 8 | CNS08C9J | AL732644 Oryza sat |
| C 33 | 94.4 | 5.3 | 157690 | 8 | CNS08CA3 | AL772425 Oryza sat |
| C 34 | 94.4 | 5.3 | 167427 | 8 | AC139174 | AC139174 Oryza sat |
| C 35 | 94.2 | 5.3 | 120926 | 2 | AC133008 | AC133008 Oryza sat |
| C 36 | 94.2 | 5.3 | 122721 | 8 | OSJN00111 | AL606660 Oryza sat |
| C 37 | 94.2 | 5.3 | 133321 | 8 | AP005306 | AP005306 Oryza sat |
| C 38 | 94.2 | 5.3 | 147461 | 8 | AP004691 | AP004691 Oryza sat |
| C 39 | 94.2 | 5.3 | 156676 | 8 | AP004839 | AP004839 Oryza sat |
| C 40 | 94.2 | 5.3 | 160665 | 8 | AP005613 | AP005613 Oryza sat |
| C 41 | 94.2 | 5.3 | 170759 | 8 | AP003271 | AP003271 Oryza sat |
| C 42 | 94 | 5.3 | 163580 | 8 | AC084767 | AC084767 Oryza sat |
| C 43 | 93.4 | 5.3 | 148848 | 8 | AP005426 | AP005426 Oryza sat |
| C 44 | 93.4 | 5.3 | 154950 | 8 | AP005429 | AP005429 Oryza sat |
| C 45 | 93.4 | 5.3 | 167353 | 8 | AP005261 | AP005261 Oryza sat |

ALIGNMENTS

RESULT 1
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DEFINITION Sequence 1 from Patent WO0078975.
ACCESSION AX063520
VERSION AX063520.1 GI:12541259
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Donaldson, I.A. and Rasmussen, T.B.
TITLE Rice sucrose synthase promoter
JOURNAL Patent: WO 0078975-A 1 28-DEC-2000;
DANISCO A/S (DK)
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1772; DB 6; Length 1772;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 TTATGGACGAGGAGTAAGTAGAGATTGTAGCCAGAAAAACAAAAACAAACACACCCG 180
QY 181 CACCTGGCAGGATCGCATCTTAGTTCGGCACATTGAGAGTCGGCAGTAGACAGTTACC 240
Db 181 CACCTGGCAGGATCGCATCTTAGTTCGGCACATTGAGAGTCGGCAGTAGACAGTTACC 240

| | | | | |
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| | Db | 181 | CACCTGGCAGGATGCATCTTAGTTCGGCACATTGAGAGGTGGCGAGTAGACGAGTTACC | 240 |
| | Qy | 241 | CTACACAACTGCTCTTCACTAGTGAGCTAGCTGCATGTTCTGTCTGCATTTACAATGCAGG | 300 |
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| | Qy | 301 | CAGCAGCTAGCAACAGTTTTGCAGGAACAATCGATAATCCATTGTGTGCAGGAGGAACATG | 360 |
| | Db | 301 | CAGCAGCTAGCAACAGTTTTGCAGGAACAATCGATAATCCATTGTGTGCAGGAGGAACATG | 360 |
| | Qy | 361 | GAGAAAAACCGGGCTGGAGACGAACCGGAGCAGCTGTACCGTAGCGTTTCTCAAAGCTGA | 420 |
| | Db | 361 | GAGAAAAACCGGGCTGGAGACGAACCGGAGCAGCTGTACCGTAGCGTTTCTCAAAGCTGA | 420 |
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| | Db | 421 | ACCCATCTGCGAAAATCCGCAGATTTGGTTGTTTCAATTCCAAATTCGAGTCCTTCAGATNG | 480 |
| | Qy | 481 | GTTGCATGTTTCAACCGTAGTACATCTGAAAAATGAAGTGTAAATACCTTTGAGAAGACT | 540 |
| | Db | 481 | GTTGCATGTTTCAACCGTAGTACATCTGAAAAATGAAGTGTAAATACCTTTGAGAAGACT | 540 |
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| | Db | 541 | TCATGGAAGCATGCCCTCGAGCGGATTTAGCTAAGAAAAAATAAATTAATGTACTTTTCGAA | 600 |
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| | Qy | 661 | GTTTAAACCGGTAAATAGTCAGATATAAAAATTTTACTATAGATCAATTTATAAATCATTTT | 720 |
| | Db | 661 | GTTTAAACCGGTAAATAGTCAGATATAAAAATTTTACTATAGATCAATTTATAAATCATTTT | 720 |
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| | Db | 721 | TAGTTGCTTTCGTTCAATTTTCTACCACTTATCAACCATAGCTCAACTGATCAATTTGCAAA | 780 |
| | Qy | 781 | TAAAGTTTACTTAAACGACATCGCTCATCACACCCAACGCTCACCGATGGTGCTCTC | 840 |
| | Db | 781 | TAAAGTTTACTTAAACGACATCGCTCATCACACCCAACGCTCACCGATGGTGCTCTC | 840 |
| | Qy | 841 | GACCACGAGTTTAGCACTTTGTGCAACAATATATGCGTGGATGAACATCTACTGATGCC | 900 |
| | Db | 841 | GACCACGAGTTTAGCACTTTGTGCAACAATATATGCGTGGATGAACATCTACTGATGCC | 900 |
| | Qy | 901 | ATGCGAATTTTAGCGTTTCGTTTCATGACGCTTCCACGSCACAGAGGCTGACGAGCAT | 960 |
| | Db | 901 | ATGCGAATTTTAGCGTTTCGTTTCATGACGCTTCCACGSCACAGAGGCTGACGAGCAT | 960 |
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| | Qy | 1021 | AGTTAGCAGAAATGCAAGGCCCATGCATATGCAATGCTATGCAACAAGTATAGTACCAGCA | 1080 |
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| | Qy | 1081 | TGATGTTAGCCAGCTAACTAATCTATCAGCAGGAGCAGNAGCTCGTGCATGTTGTAT | 1140 |
| | Db | 1081 | TGATGTTAGCCAGCTAACTAATCTATCAGCAGGAGCAGNAGCTCGTGCATGTTGTAT | 1140 |
| | Qy | 1141 | GCATTTCTCCAGTAATCTAGTGGTAAATTTTCAACCCAAAGCGTTGCTCATATGGACAGT | 1200 |
| | Db | 1141 | GCATTTCTCCAGTAATCTAGTGGTAAATTTTCAACCCAAAGCGTTGCTCATATGGACAGT | 1200 |
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| | Db | 1201 | AATTAGTAATATTACCAAGGTTCAATCCCGTTTACCTGACCAATACTACTCACGAATG | 1260 |
| | Qy | 1261 | GTATCTCTGCTTTCGTTTAAACCGTTGGTAAACCGCAAAAATPAGACAAAATTTGTCAA | 1320 |

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|----|------|---|------|
| Db | 1261 | GTATCTCTGGTTTTTCGTTAAACCGTTGGTTAAACCCAGCAAAATAGACAAATTTGTCAA | 1320 |
| Qy | 1321 | AATTTTAAATTTTAGTTTTTTTTTAACTTAGCCGGGAAACCTTTGAAGATTGTGCTGTGC | 1380 |
| Db | 1321 | AATTTTAAATTTTAGTTTTTTTTTAACTTAGCCGGGAAACCTTTGAAGATTGTGCTGTGC | 1380 |
| Qy | 1381 | AGCTGTCTCTGGGAAGGACGGTTTTTGGTTGGGATTGTGAACCTGTGCACTTCATT | 1440 |
| Db | 1381 | AGCTGTCTCTGGGAAGGACGGTTTTTGGTTGGGATTGTGAACCTGTGCACTTCATT | 1440 |
| Qy | 1441 | TTTGAACAGATATTAGTGTCAACAGACAAATGCCAACCGCATTTTTTCTGTTTACCGGCAA | 1500 |
| Db | 1441 | TTTGAACAGATATTAGTGTCAACAGACAAATGCCAACCGCATTTTTTCTGTTTACCGGCAA | 1500 |
| Qy | 1501 | GCTGAAAGCTTTTACGATCCCCATACCGCCGTTGTGTCAAAACCTGCCAAAGAAAGACGACGA | 1560 |
| Db | 1501 | GCTGAAAGCTTTTACGATCCCCATACCGCCGTTGTGTCAAAACCTGCCAAAGAAAGACGACGA | 1560 |
| Qy | 1561 | GAACACAGTGTCTATTTTGTGGTGGAAAGCCAAAGTAAAGTAAACAGAGATGGAAGATAGT | 1620 |
| Db | 1561 | GAACACAGTGTCTATTTTGTGGTGGAAAGCCAAAGTAAAGTAAACAGAGATGGAAGATAGT | 1620 |
| Qy | 1621 | GAGGACCAGGAGTGAAGCAGGGGACACATGGGCCACGCCCTCCCTGCACATTTTCGTGTA | 1680 |
| Db | 1621 | GAGGACCAGGAGTGAAGCAGGGGACACATGGGCCACGCCCTCCCTGCACATTTTCGTGTA | 1680 |
| Qy | 1681 | TAAATACAGTGGATGCATCGCTCTCCAGCATCCATCGGTTCTCTGCTCTGTTCAATCCA | 1740 |
| Db | 1681 | TAAATACAGTGGATGCATCGCTCTCCAGCATCCATCGGTTCTCTGCTCTGTTCAATCCA | 1740 |
| Qy | 1741 | TAGAGTTTCCCTCTCTTCTCCCTTCAGTGCAG | 1772 |
| Db | 1741 | TAGAGTTTCCCTCTCTTCTTCAGTGCAG | 1772 |

| | |
|------------|---|
| RESULT 3 | |
| AP004988 | 168173 bp DNA linear |
| LOCUS | Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7, |
| DEFINITION | BAC clone:BL056G08. |
| ACCESSION | AP004988.3 GI:24060020 |
| VERSION | |
| KEYWORDS | |
| SOURCE | Oryza sativa (japonica cultivar-group) |
| ORGANISM | Oryza sativa (japonica cultivar-group) |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; |
| | Ehrhartoideae; Oryzeae; Oryza. |
| 1 | |
| REFERENCE | Sasaki, T., Matsumoto, T. and Yamamoto, K. |
| AUTHORS | Oryza sativa nipponbare (GAS) genomic DNA, chromosome 7, BAC |
| TITLE | Clone:BL056G08 |
| JOURNAL | Published Only in Database (2002) |
| REFERENCE | 2 (bases 1 to 168173) |
| AUTHORS | Sasaki, T., Matsumoto, T. and Yamamoto, K. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (27-MAR-2002) Takuji Sasaki, National Institute of |
| | Agricultural Sciences, Rice Genome Research Program; Kannondai |
| | 2-1-2, Tsukuba, Ibaraki 305-8602, Japan |
| | (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/ , |
| | Tel:81-298-38-7441, Fax:81-298-38-7458) |
| | On Oct 16, 2002 this sequence version replaced gi:22212589. |
| | Genes were predicted from the integrated results of the following: |
| | GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH |
| | (http://www.softberry.com/), GeneMark hmm |
| | (http://opal.biology.gatech.edu/GeneMark/), GlimmerM |
| | (http://www.tigr.org/tdb/glimmer/glmr form.html), RiceHMM |
| | (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor |
| | (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 |
| | (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 |
| | (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The |
| | genomic sequence was searched against NCBI NonRedundant Protein |
| | database, nrftp://ncbi.nlm.nih.gov/blast/db) and the cDNA |

sequence database at RGP or DBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of B1056G08 clone has an overlap with P0616D06 (DBJ: AP005198) at 5' end and an overlap with P0552F09 clone (DBJ: AP004308) at 3' end and an overlap with P0560B08 clone (DBJ: AP004309) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/genomeSeq.html>.

FEATURES

source

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LOCUS AX063525 1686 bp DNA linear PAT 24-JAN-2001
 DEFINITION Sequence 6 from Patent WO0078975.
 ACCESSION AX063525
 VERSION AX063525.1 GI:12541264
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 1
 REFERENCE
 1 Donaldson, I.A. and Rasmussen, T.B.
 TITLE Rice sucrose synthase promoter
 JOURNAL Patent: WO 0078975-A 6 28-DEC-2000;
 DANISCO A/S (DK)
 FEATURES
 Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DEFINITION Sequence 6505 from Patent WO03000898.

AX656635 2000 bp DNA linear PAT 22-MAR-2003
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5.9%; Score 103.8; DB 8; Length 161865;

Query Match

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Best Local Similarity 93.9%; Pred. No. 2.1e-14;
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RESULT 8
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DEFINITION Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0039K24,
complete sequence.
ACCESSION AL606637
VERSION AL606637.3 GI:32480037
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Feng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J.,
Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
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Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
NATURE 420 (6913), 316-320 (2002)
22337377
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REFERENCE 2
AUTHORS Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q., Hu,X.,
Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J., Zhang,L.,
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Hong,G.F.
Direct Submission
Submitted (08-SEP-2001) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSJNBa0039K24.
On Jul 8, 2003 this sequence version replaced gi:21912475.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics
Assembly program: phrap
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This is a complete sequence.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (http://www.softberry.com/),
genescan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM
(http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean
Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the
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Location/Qualifiers
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Query Match 5.6%; Score 99.8; DB 8; Length 173770;
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RESULT 9
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LOCUS Oryza sativa chromosome 3 BAC clone OSUNB0069P02, complete
DEFINITION
AC145780
VERSION AC145780.2 GI:50872484
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 88044)
AUTHORS Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,
Overton II,L., Tsitrin,T., Kim,M., Bera,J., Jin,S., Fadrosch,D.W.,
Tallon,L., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.,
Riedmuller,S.B., Uterbach,T., Feldblyum,T., Yang,Q., Haas,B.,
Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and
Fraser,C.
TITLE Oryza sativa ssp. japonica cv. Nipponbare OSUNB0069P02 BAC genomic
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 88044)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 88044)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jul 31, 2004 this sequence version replaced gi:33285037.
FEATURES
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1. .88044
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="3"
/clone="OSUNB0069P02"
/notes="japonica cultivar-group"

ORIGIN
Query Match 5.6%; Score 99.2; DB 8; Length 88044;
Best Local Similarity 85.9%; Pred. No. 2.9e-13;
Matches 110; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ACTTTAGATAATAAGTCAAGTAAAGTCAAAATTCCTTATATATGGGAC-TTAT 60
Db 62909 ACTTTGGATAATAAGTCAAGTAAAGTCAAAATTCCTTATATATGGGAC-TTAT 62968
Qy 61 AGACGAGTGTCAACAGTCAAGTAAAGTCAAAATTCCTTATATATGGGAC-TTAT 120
Db 62969 AGACGAGTGTCAACAGTCAAGTAAAGTCAAAATTCCTTATATATGGGAC-TTAT 120
Qy 121 TTATGGGA 128
Db 63029 AAGTAGGA 63036

FEATURES
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gene 1532..2626
/notes="transposon02 TNP2-like transposon protein gi|4"
CDS 1532..2626
/notes="Hypothetical protein"
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/notes="Similar to pir||T46123 hypothetical protein"

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RESULT 10
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LOCUS
DEFINITION
AC090485
VERSION AC090485.3 GI:14495364
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 159636)
AUTHORS de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K., King,L.,
Nascimento,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
Miller,B., Kuit,K., Cumnius,D.M., Rodriguez,S., Balija,V., Shah,R.,
Bahret,A., Yang,C., Bell,M., Palmer,L., O'Shaughnessy,A., Dedhia,N.
and McCombie,W.R.
TITLE Genomic Sequence for Oryza sativa, Nipponbare strain, clone
OSUNB0067N01, from chromosome 3, complete sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159636)
AUTHORS McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
REFERENCE 3 (bases 1 to 159636)
AUTHORS McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
REFERENCE 4 (bases 1 to 159636)
AUTHORS Palmer,L.E., de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K.,
King,L., Nascimento,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
Miller,B., Kuit,K., Cumnius,D.M., Rodriguez,S., Balija,V., Shah,R.,
Bahret,A., Yang,C., Bell,M., O'Shaughnessy,A., Dedhia,N. and
McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY
11724, USA
REMARK
COMMENT
On Jun 20, 2001 this sequence version replaced gi:14209722.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.
FEATURES
source
1. .159636
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="3"
/clone="OSUNB0067N01"
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/notes="transposon02 TNP2-like transposon protein gi|4"
1532..2626
/notes="Hypothetical protein"
1532..2626
/notes="OSUNB0067N01.1"
/notes="Similar to pir||T46123 hypothetical protein"

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LAHGAALVPRHGGGCAASRKLSEYRLFAEHLIDPDORAVAAALASGSLRDPVR
GLLAAYAEATANAFSLCSHLLQIEHLRYRPLKTLKRLASDVGVSLADVSAALG
VQPTALAAQRLREVQAGDGLRLDAGKARHRSVRLRALSVSFVAVAV
VAVGACIGVHLAFAAFPMWGSFPAWGERFSGRAARLALVLEAAKGYIILNRM
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complement(3166..5556)
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/notes="Putative signal peptidase"
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5366..5452,5534..5556))
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/gene="OSJNBa0067N01.3"
/notes="Unknown protein with similarity to
methyitransferases and transcriptional regulators"
Join(7459..9132,9247..9330,9641..9745,9839..9947,
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/gene="OSJNBa0067N01.3"
/notes="Similar to dbj|BAA88534.1| (AP000969) Similar to
Arabidopsis thaliana DNA chromosome 4, BAC clone T51u19
(AL049481) [Oryza sativa] Identities = 571/759 Evalue=
0.0; Similar to sp|P25583|KAR4 YEAST KARYOGAMY PROTEIN
KAR4 Identities = 98/328 Evalue= 2e-27"
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methyitransferases and transcriptional regulators"
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CKEERCNTNKRKSGAMGDDSDSRVSHETEVHFNDDKQKAVEIKNILDHGVGQ
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SQDSKASDSEWNAQERQDGGFGRVGYRDRFRGSRSTYGSRYDTSLSIE
IRPNNSLDFRSGSVGRYDVGARHVDVYTGNGDKVYNSEPDQSGSASMLSQPPQH
GHKDRPFRGGRGRNDRSQRVGVTLPIMPPFPPLPGPPGMQHGNIHPSGPH
LLPGVFPVPPPGGILLMPGARGVDVNMVSLPPLPPVAGEHSTPGMGAGPNIHL
NPGSGIGAPTNGSLSHQLTQSGREHVGKPPVGGWTPNRSQPTKAPSRGEQN
DYSQVDTGMGPONFIRELDTLSVAEDYPKLRELTQKDEIVAKSASPMYVKCDLR
QVLSPEPGETEDVILDPWPEEYVAPGTTDHTLEYNGEIEINLKTAEADTSPF
VFLWQGVGLSQGQCLCKWGRFRCEDVCWTKNKSATPSLRHDSHTILQSHKEHC
LMGKGTGVRSDTHVHANIDTIIIDPTDGSKKEDDMTRIIIEHFALGRRLLEL
FGEDHNRFPWTLTGKLSYSNFKNEAYVKNFADKDKGVQWQGGNPPPEAPHLVVTTT
ELEGRLPKSPPHK"
14781..14815
/notes="misc rep03 similar to Rat tandem repeat mRNA"
complement(16651..16787)
/notes="Galign_O12 MITE element from gb:U72728 Oryza 1"
complement(17170..17328)
/notes="Wanderer_Os5 MITE element from gb:X13679 Oryza"
19417..20916
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/notes="Putative retroelement"
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/gene="OSJNBa0067N01.4"
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170/488 Evalue= 3e-53"
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RNKPKREASASSMGVLEKAGDKKAIWEDSDNESAAQLVKLQKMEIDRELALRV
QLESQPKQIQLQDVAGMGLEGIRAOAGEGENKTKTOEGMAKSGTSORVEN
DSEVITDEDEPRVOLVGSSENMESQSSDFAVGVVLSQTDDEMTKEKKKSLRLM
EKDKKAAADAAARKEALNFIKDKCALEAVDTNLLNKLINLEKARINFLKELKNTSQ
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EIFVTPKSGKNEKKTKKKS"
21438..24126
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/gene="OSJNBa0067N01.5"
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POL POLYPROTEIN [CONTAINS"
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NKAPGDPVDFYFHYKFWYLLKDDLMELIIDPMKKRIGVERLNYGIVTILPKCKEAGI
LFKIDFKVYNIKMSVYKMKAKGFPDINCDWTLKVVKGKVAIRVNYQIGHYFTT
HKLQOGDPLSPLLNIAADALTLIKRAEQOGLIKGLGDMVRGVDILQADDTTC
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complement(25940..26286)
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/notes="Wanderer_Os1 MITE element from gb:IL28995 Oryza"
complement(28675..29018)
/notes="Castaway_Os2 MITE element from gb:D26547 Rice"
30964..31259
/notes="G340 Oryza sativa repetitive element G340 gi|5"
34133..36012
/gene="OSJNBa0067N01.6"
/notes="Putative anion transporter"
join(34133..35347,35444..35633,35744..36012)
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/notes="Similar to gb|AAC24385.1| (U089959) Hypothetical
protein [Arabidopsis thaliana] Identities = 333/556
Evalue= e-174"
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Query Match 5.6%; Score 99; DB 8; Length 159636;
Best Local Similarity 91.3%; Pred. No. 3.2e-13;
Matches 105; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTACAGTACAGAGAAAAATAATAATAATTCAAAATTTTTTAATA 60
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Db 104069 ACTTTGGAATAATAAGTACAGAGAAAAATAATAATAATTCAAAATTTTTTAATA 104010
|||||

QY 61 AGACGAGTGTGTCACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 115
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Db 104009 AAACGAATGTCACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 103955
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RESULT 11

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EAQLINDIGSKSDIDDESSRARCFFSHELPIADDSQSCDESPHRTVFLVLPGESD
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MSGELMARLVLDTHFGVDDHGAGDGLYGLFARFDRDGDGKVLGHEFRAEMKEVWL
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26625..26909,27113..27324,27989..28060))
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26625..26909,27113..27320))
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AU165589(E2727),AU101718(S21081),AU057034(S21081),
AU165588(E2727)
contains full-length cDNA(s): AK064774,AK099206,AK065126"
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RKILDKHRHALLVDGVSSICALDPRMDGVDVLTGSQKALSPLTGLTGIVCASP"

Query Match 5.6%; Score 98.8; DB 8; Length 121202;
Best Local Similarity 83.6%; Pred. No. 3.6e-13;
Matches 112; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ACTTTAGATTAATAAGTCACTACAGAAAATAATAATAATTCCTTATATATGGAACCTATA 120
DB 111538 ATTGTAGATTAATAAGTCACTACAGAAAATAATAATAATAATTCCTTATATATGGAACCTATA 111479

QY 61 AGACGAGTGTGCTCAACAGTCAAGTAACTCAAAATTCCTTATATATGGAACCTATA 120
DB 111478 AGACGAGTGTGCTCAACAGTCAAGTAACTCAAAATTCCTTATATATGGAACCTATA 111419

QY 121 TTATGGACGCGAGG 134
DB 111418 GAGTAGGAATCAGG 111405
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RESULT 12
AP003883/c
LOCUS
ORyza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
BAC clone:OJ1134_H03.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
ORyza sativa (japonica cultivar-group)
ORyza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1
Sasaki,T., Matsumoto,T. and Yamamoto,K.
ORyza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
clone:OJ1134_H03
Published Only in Database (2001)
2 (bases 1 to 135914)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (09-JUL-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakiana@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Feb 4, 2004 this sequence version replaced gi:37497091.
Genes were predicted from the integrated results of the following:
GENSCAN (http://ccr-081.mit.edu/GENSCAN.html), FGENSEH
GENSCAN (http://softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://opal.tigr.org/tdb/glimmer/glmr form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI Nonredundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DBJ. Protein homologues of the coding
regions were searched against NCBI Nonredundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
a probable 'hypothetical' protein and is included as a
miscellaneous feature of the sequence.
The orientation of the sequence is from M13rev to -21M13 of the BAC
clone. This sequence of OJ1134_H03 clone has an overlap with
OJ1506_F01 clone (DBJ: AP004190) at 5' end and an overlap with
OSJNBa025222 (DBJ: AP005245) at 3' end. The sequence was generated
by combining Monsanto and RGP-Japan sequencing data. Detailed
information on overlap and assembly quality together with
annotation of this entry is available at
http://rgp.dna.affrc.go.jp/GenomeSeq.html.
FEATURES
Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
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5..3043
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gene

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CDS
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ARRGGVDAADSDDDDDCCYHLOQDEGAAGSTATPAAARAPLPAFLNCI
PTCCGDDGDDSDVEAGTTADIDAVALRIGLPAGGTEADLLSLGAGVEHEE
EDCKVGGGDDVPLGRFSSTPIGKLNKGWYIPTPSOILLIPTQFSCVCPKT
ENRYNMOMHMGHSGSOYKGPESLPGVQPTAMLRPLCYCCAAGCRNIDHPRARPLK
DPTLTQYKRXHGLKPFICRCKGFAVKGDMRTHKNCGLWYLCGSEFKHRSLS
KHARAFGAHTALDADDGDAVDADAVVRPSSMAASSLQPPR"
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join(<3604..3657,4767..5096,6431..>6547)
/gene="OJ1134_H03.2"
/note="start and end point are not identified"
CDS
join(3604..3657,4767..5096,6431..6547)
/gene="OJ1134_H03.2"
/note="predicted by GENSCAN etc."
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/protein_id="BAD08820.1"
/db_xref="GI:42407671"
/translation="MTIDCRHWHACMYIINRLLEINFRRLKSTREKLIQOAS
LDMYPLLTIEWISLHILSQSLTPSOGLVVGLDRSPAAGVGLNATDPVSPPP
SRADLVGAATTNAAAGLGRCSDEGWSLGAIVGSSATMTTSDVCGSDDDSGGSCSD
DGGSG"
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/note="start and end point are not identified"
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/note="predicted by FGENSEH etc."
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complement(12581..17788)
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CDS
pseudogene, ORF stop194 - rice tungro bacilliform virus"
/pseudo
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Matches 112; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 ACTTTAGATATAAGTAGTACAGTAAATAAATAAATTCCTTATATATGGACTTATA 120
Db 8807 ATTGTAGATATAAGTAGTACAGTAAATAAATAAATTCCTTATATATGGACTTATA 8748
QY 61 AGACGAGTGGTCAACAGTACAGTAAATAAATAAATTCCTTATATATGGACTTATA 120
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Matches 106; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Db |||||
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QY 61 AGACGAGTGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATATATGCGCTAT 119
Db |||||
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RESULT 14
AE017105/c

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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) DNA linear PLN 06-JUN-2003
300029 bp chromosome 10, section 59 of
77 of the complete sequence.
ACCESSION
AE017105 AE016959
VERSION
AE017105.1 GI:31432655
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriartoideae; Oryzaceae; Oryza.
SOURCE
1 (bases 1 to 300029)
The Rice Chromosome 10 Sequencing Consortium
In-depth view of structure, activity, and evolution of rice
chromosome 10
JOURNAL
Science 300, 1566-1569 (2003)
REFERENCE
2 (bases 1 to 300029)
Buell,C.R., Wing,R.A., McCombie,W.R., Messing,J. and Yuan,Q.
Direct Submission
Submitted (05-MAY-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
This is the pseudomolecule for rice chromosome 10, which was
constructed by resolving discrepancies between overlapping BACs,
trimming the overlap regions, and linking the unique sequences to
form a contiguous sequence. Genes in individual BAC clone were
identified by a combination of several methods: Gene prediction
programs, searches of the complete sequence against a peptide
database and EST databases. Genes with similarity to other proteins
are named after the database hits. Genes without significant
peptide similarity but with EST similarity are named as unknown
proteins. Genes without protein or EST similarity, that are
predicted by more than two gene prediction programs over most of
their length are annotated as hypothetical proteins. Genes
encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
FEATURES
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VERSION      AX656799.1  GI:29159613
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SOURCE       Oryza sativa
ORGANISM     Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1
AUTHORS      Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
             Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE        Plant genes involved in defense against pathogens
JOURNAL      Patent: WO 03000898-A 6669 03-JAN-2003;
             Syngenta Participations AG (CH)
FEATURES     Location/Qualifiers
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Best Local Similarity 90.4%; Pred. No. 8.e-13;
Matches 104; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY      1  ACTTTAGATAATAAGTAAGTCACAAGAAAAATAAATAATTCCTTATATATGGGAC 60
Db      595  ACTGTAGATAATAAGTAAGTCACAATAATAATAATAATTCCTTATATATGGGAC 536
QY      61  AGACGAGTGGTCAACAGTACAGTAAACCTCAAAATTCCTTATATATGGGAC 115
Db      535  AGAGGAGTGGTCAACACATTGTAAGTAAACCTCAAAATTCCTTATATATGGGAC 481

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Search completed: November 17, 2004, 13:09:56
Job time : 7355 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 09:30:30 ; Search time 824 Seconds
(without alignments)

11288.804 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataaagtaag.....ctcttccttcagtgcaag 1772

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 1772 | 100.0 | 1772 | 4 | Aaf24785 Nucleotid |
| 2 | 1772 | 100.0 | 1803 | 4 | Aaf24787 Nucleotid |
| 3 | 1772 | 100.0 | 2668 | 4 | Aaf24791 Complete |
| 4 | 1686 | 95.1 | 1686 | 4 | Aaf24790 Nucleotid |
| 5 | 1082.4 | 61.1 | 2000 | 8 | Ada73179 Rice gene |
| 6 | 97.4 | 5.5 | 2000 | 8 | Ada73343 Rice gene |
| 7 | 87.8 | 5.0 | 2000 | 12 | Adj40841 Plant CDN |
| 8 | 86 | 4.9 | 86 | 4 | Aaf24788 Nucleotid |
| 9 | 85.8 | 4.8 | 5579 | 6 | Aal46958 Rice lesi |
| 10 | 85.4 | 4.8 | 2000 | 8 | Ada72806 Rice gene |
| 11 | 84.2 | 4.8 | 2000 | 12 | Adj41087 Plant CDN |
| 12 | 83.2 | 4.7 | 900 | 12 | Adg27907 Rice vari |
| 13 | 83 | 4.7 | 2000 | 10 | Adc08414 Rice DNA |
| 14 | 81.8 | 4.6 | 2000 | 8 | Ada73166 Rice gene |
| 15 | 81.6 | 4.6 | 2000 | 8 | Ada71497 Rice gene |
| 16 | 81.6 | 4.6 | 2000 | 8 | Ada73455 Rice gene |
| 17 | 81.6 | 4.6 | 2000 | 8 | Ada71498 Rice gene |
| 18 | 81 | 4.6 | 2000 | 8 | Ada72521 Rice gene |
| 19 | 80.4 | 4.5 | 2000 | 8 | Ada72089 Rice gene |
| 20 | 80.4 | 4.5 | 12120 | 6 | Aas96695 Rice DMT1 |
| 21 | 80.4 | 4.5 | 12120 | 11 | Adm39550 DMT polyn |

ALIGNMENTS

RESULT 1

AAP24785

ID AAF24785 standard; DNA; 1772 BP.

XX AAF24785;

AC AAF24785;

DT 20-APR-2001 (first entry)

XX Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter.

DE Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression;

KW transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.

OS Oryza sativa.

XX WO200078975-A2.

XX 28-DEC-2000.

PF 15-JUN-2000; 2000WO-GB002641.

PR 17-JUN-1999; 99GB-00014210.

XX (DANI-) DANISCO AS.

PI Donaldson IA, Rasmussen TB;

XX WPI; 2001-071398/08.

PT Rice sucrose synthase 3 promoter obtainable from plant genus Oryza,

PT useful for expressing nucleotide sequence of interest in specific tissue

PT or cell type e.g. endosperm.

XX Claim 1; Page 142; 144pp; English.

XX The present sequence represents a rice sucrose synthase 3 (RSus3)

CC promoter. The RSus3 promoter has low homology with the RSus1 and RSus2

CC promoters (7.7% and 4.8%, respectively). In addition, apart from

CC conserved TATA box and intron splice sites, they have no motifs in

CC common. The promoter can be used to prepare a product of interest,

CC especially in the endosperm of a transgenic plant. Preferably, the

CC promoter is used to cause expression of a nucleotide of interest that can

CC affect carbohydrate metabolism, such as sucrose metabolism, in a plant

CC tissue

Ada72445 Rice gene
Ada71685 Rice gene
Ada71634 Rice gene
Adj41150 Plant CDN
Ada73432 Rice gene
Ada71850 Rice gene
Ada72700 Rice gene
Ada73195 Rice gene
Ada73460 Rice gene
Adj41154 Plant CDN
Ada72153 Rice gene
Adj40722 Plant CDN
Adj40664 Rice gene
Adp03394 Rice MITE
Adj41176 Plant CDN
Ada71503 Rice gene
Ada71548 Rice gene
Adj40731 Plant CDN
Ada71778 Rice gene
Ada73205 Rice gene
Ada72764 Rice gene
Ada71501 Rice gene
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Ada71955 Rice gene

| | |
|----------|--|
| RESULT 2 | |
| AAF24787 | |
| ID | AAF24787 standard; DNA; 1803 BP. |
| XX | |
| XX | |
| AC | AAF24787; |
| XX | |
| DT | 20-APR-2001 (first entry) |
| XX | |
| DE | Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter. |
| XX | |
| KW | Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; |
| KW | transgenic plant; carbohydrate metabolism; sucrose metabolism; ss. |
| XX | |
| OS | Oryza sativa. |
| XX | |
| PN | WO200078975-A2. |
| XX | |
| PD | 28-DEC-2000. |

[illegible]

| | | | | | |
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| Db | 1321 | AAATTTAAATTTT | TAGTTTTTTT | TAACTAGCCGGGAAACCTTGAAGTTTGTGCTGTCG | 1380 |
| Qy | 1381 | AGCTGTCTCTGGGAGGACGGTTTTTGGTTGGGATTTGTGAACCTCGTTACTGCACTTCATT | 1440 | | |
| Db | 1381 | AGCTGTCTCTGGGAGGACGGTTTTTGGTTGGGATTTGTGAACCTCGTTACTGCACTTCATT | 1440 | | |
| Qy | 1441 | TTTGAACAGATATTAGTGTCAACAGACAAATGCCAACGCAATTTTTTTCTGTTTACCGGCAA | 1500 | | |
| Db | 1441 | TTTGAACAGATATTAGTGTCAACAGACAAATGCCAACGCAATTTTTTTCTGTTTACCGGCAA | 1500 | | |
| Qy | 1501 | GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGAAACCTGCCAAGAAAGACAGCA | 1560 | | |
| Db | 1501 | GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGAAACCTGCCAAGAAAGACAGCA | 1560 | | |
| Qy | 1561 | GAACAAGGTGTCATTTTGTGTGGTGGAAAGCCAAAGTAAAGTAAACAGAAGATGGGAAGATAGT | 1620 | | |
| Db | 1561 | GAACAAGGTGTCATTTTGTGTGGTGGAAAGCCAAAGTAAAGTAAACAGAAGATGGGAAGATAGT | 1620 | | |
| Qy | 1621 | GAGGACCAAGGACGTGAGCAGGGGACACATGGGCCACGCTCCCTGCACATTTTCGTGTGA | 1680 | | |
| Db | 1621 | GAGGACCAAGGACGTGAGCAGGGGACACATGGGCCACGCTCCCTGCACATTTTCGTGTGA | 1680 | | |
| Qy | 1681 | TAAATACAGGTGGATGCATCGCTCTCCAGCATCCATCGGTTCTCTGCTCTGTTTCATCCA | 1740 | | |
| Db | 1681 | TAAATACAGGTGGATGCATCGCTCTCCAGCATCCATCGGTTCTCTGCTCTGTTTCATCCA | 1740 | | |
| Qy | 1741 | TAGAGTTTCCTCTCTTCTCTCTCCCTCAGTGGGAAG | 1772 | | |
| Db | 1741 | TAGAGTTTCCTCTCTTCTCTCTCCCTCAGTGGGAAG | 1772 | | |

RESULT 4

| | |
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| AAAF24790 | AAAF24790 standard; DNA; 1686 BP. |
| XX | |
| XX | |
| AC | AAAF24790; |
| XX | |
| DT | 20-APR-2001 (first entry) |
| XX | |
| DE | Nucleotide sequence of a sucrose synthase 3 (RSus3) promoter fragment. |
| XX | |
| XX | Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; |
| KW | transgenic plant; carbohydrate metabolism; sucrose metabolism; ss. |
| KW | |
| XX | |
| OS | Oryza sativa. |
| XX | |
| XX | WO200078975-A2. |
| PN | |
| XX | |
| PD | 28-DEC-2000. |
| XX | |
| XX | |
| PF | 15-JUN-2000; 2000WO-GB002641. |
| XX | |
| XX | |
| PR | 17-JUN-1999; 99GB-00014210. |
| XX | |
| PA | (DANI-) DANISCO AS. |
| XX | |
| PI | Donaldson IA, Rasmussen TB; |
| XX | |
| XX | |
| XX | WPI; 2001-071398/08. |
| DR | |
| XX | |
| PT | Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, |
| XX | useful for expressing nucleotide sequence of interest in specific tissue |
| PT | or cell type e.g. endosperm. |
| PT | |
| XX | |
| PS | Disclosure; Page 144; 144pp; English. |
| XX | |
| XX | |
| CC | The present sequence represents a rice sucrose synthase 3 (RSus3) |
| CC | promoter fragment. The RSus3 promoter has low homology with the RSus1 and |
| CC | RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from |
| CC | conserved TATA box and intron splice sites, they have no motifs in |

| | | | | |
|----|------|-----------------------|--|------|
| QY | 1209 | ATATTACCAAGGTTCA | CAATCCCGTTACCTGACCAAAATACTACTACAGAAATGGTATCTCT | 1368 |
| Db | 541 | ATATTACCAAGGTTCA | CAATCCCGTTACCTGACCAAAATACTACTACAGAAATGGTATCTCT | 600 |
| QY | 1269 | GGTTTTTCGTTAAACCGTTG | TAAACAGCAAAAATAGACAAAATTTGTCAAATTTTAA | 1328 |
| Db | 601 | GGTTTTTCGTTAAACCGTTG | TAAACAGCAAAAATAGACAAAATTTGTCAAATTTTAA | 660 |
| QY | 1329 | ATTTTAG - TTTT | TTTTTTTAACTTAGCGCGAAACCTTGAAGTTTGTGCTCGAGCTGT | 1386 |
| Db | 661 | ATTTTAGTTTTTTTTTTT | TTAACTTAGCGCGAAACCTTGAAGTTTGTGCTCGAGCTGT | 720 |
| QY | 1387 | CCTGGGAAGACGGTTTTGGT | TGGGATGTGAACCTGGTTACTGCACTTCATTTTGA | 1446 |
| Db | 721 | CCTGGGAAGACGGTTTTGGT | TGGGATGTGAACCTGGTTACTGCACTTCATTTTGA | 780 |
| QY | 1447 | CAGATATTAGTGCAACAGACA | AAATGCCAAGCATTTTTTCTGTTTACCGGAAGCTGAA | 1506 |
| Db | 781 | CAGATATTAGTGCAACAGACA | AAATGCCAAGCATTTTTTCTGTTTACCGGAAGCTGAA | 840 |
| QY | 1507 | GCTTTTACGATCCCATAC | CGCGTGTCTGCAAAACCTGCCAAGAAAGACAGCAGAAACA | 1566 |
| Db | 841 | GCTTTTACGATCCCATAC | AGCGTGTCTGCAAAACCTGCCAAGAAAGACAGCAGAAACA | 900 |
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| Db | 901 | GGTGTCATTTTGTG | TGGGAAGCCAGTAAAGTAAACAGAAAGTGAAGATAGTAGGAC | 960 |
| QY | 1627 | CAGGGAGTAGGCAAGGGG | ACACATGGCCACGCTCCCTGCAATTTTGTGTATAAATA | 1686 |
| Db | 961 | CAGGGAGTAGGCAAGGGG | ACACATGGCCACGCTCCCTGCAATTTTGTGTATAAATA | 1020 |
| QY | 1687 | CAGGTGGATGCATCGCT | CTCCAGCATCCATCGGTTCTCTGTCTGTTCATCCATAGAGT | 1746 |
| Db | 1021 | CAGGTGGATGCATCGCT | CTCCAGCATCCATCGGTTCTCTGTCTGTTCATCCATAGAGT | 1080 |
| QY | 1747 | TTCCCTCCTCTTCTCCT | TTCACTAGTCAAG | 1772 |
| Db | 1081 | TTCCCTCCTCTTCTCCT | TTAGTGAAG | 1106 |

| | |
|----|--|
| PT | bacterial, fungal or viral infection by determining or detecting plant gene expression. |
| PT | |
| XX | |
| PS | Claim 27; SEQ ID NO 6659; 899pp; English. |
| XX | |
| CC | The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention. |
| CC | |
| CC | |
| XX | |
| SQ | Sequence 2000 BP; 627 A; 386 C; 393 G; 594 T; 0 U; 0 Other; |
| | |
| | Query Match 5.5%; Score 97.4; DB 8; Length 2000; |
| | Best Local Similarity 90.4%; Pred. No. 3e-15; |
| | Matches 104; Conservative 0; Mismatches 11; Indels 0; Gaps 0 |
| QY | 1 ACTTTAGATATAAAGTAGTCACAAAGAAAAATAAATAATTCCTTCAAAATTTTTTAATA 60 Db 595 ACTGTAGATAATAAAGTAGTCACAAAATAAAATAAATAATTCCTTCAAAATTTTTGAATA 536 QY 61 AGACGAGTGGTCAAACAGTAGTCAAGTAAAAACTCAAATTCCTTATATTATGGGAC 115 Db 535 AGAGGAGTGTCAAACAATTGTAAGTAAAAACTCAAATTCCTTATATTATGGGAC 481 |
| QY | |
| Db | |
| QY | |
| Db | |

PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to

DR WPI; 2002-372312/40.
 XX P-PSDB; AAO17798.
 PT Rice-originated gene, Spi7, that inhibits lesion formation and is
 PT applicable in improving heat stress of plants thus leading to prevention
 PT of lesion formation, for developing new breeds of plants for agriculture
 XX and horticulture.
 XX Claim 1; Page 30-40; 53pp; Japanese.
 XX
 CC The present invention provides the protein and coding sequences of rice
 CC lesion formation inhibitor Spi7. The protein improves the heat stress of
 CC the plant, and can be used in the development of new breeds of plants for
 CC agriculture and horticulture. The present sequence is the coding sequence
 CC of the invention
 XX
 SQ Sequence 5579 BP; 1453 A; 1272 C; 1235 G; 1619 T; 0 U; 0 Other;
 Query Match 4.8%; Score 85.8; DB 6; Length 5579;
 Best Local Similarity 88.2%; Pred. No. 6.2e-12;
 Matches 105; Conservative 0; Mismatches 12; Indels 2; Gaps 1;
 QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAAATAATTCCTTATATATGGGACTTAT 60
 DB 2257 ACTTTAGATAATAAGTAAGT--CAAAAAGAGATAAATAATTTTAAATTTTAAATA 2314
 QY 61 AGACGAGTGTGTCACAGTACAGTACAAAGTAACTCAAAATTCCTTATATATGGGACTTAT 119
 DB 2315 AGACGAGTGTGTCACAGTACAAAGTCAAAATAAACTCAAGATCCCTTATATATGGGATAAT 2373
 RESULT 10
 ADA72806/c
 ID ADA72806 standard; DNA; 2000 BP.
 XX
 AC ADA72806;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Rice gene, SEQ ID 6131.
 XX
 KW Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 XX
 OS Oryza sativa.
 XX
 PN WO2003000898-A1.
 XX
 PD 03-JAN-2003.
 XX
 PF 22-JUN-2001; 2001WO-IB001105.
 XX
 PR 22-JUN-2001; 2001WO-IB001105.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 DR
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX
 PS Claim 27; SEQ ID NO 6131; 899pp; English.
 XX
 CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX

SQ Sequence 2000 BP; 575 A; 481 C; 470 G; 467 T; 0 U; 7 Other;

Query Match 4.8%; Score 85.4; DB 8; Length 2000;
 Best Local Similarity 89.6%; Pred. No. 4.9e-12;
 Matches 103; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAAATAATTCCTTATATATGGGACTTAT 60

DB 624 ACTTTGAATAATAAGTAAGTCACAGAGAAAATAAATAATTTTAAATTTTAAATA 566

QY 61 AGACGAGTGTGTCACAGTACAGTACAAAGTAACTCAAAATTCCTTATATATGGGACT 115

DB 565 AGACGAGTGTGTCACAGTACAGTACAAAGTCAAAATTCCTTATATATGGGACT 511

RESULT 11

ADJ41087/c

ID ADJ41087 standard; cDNA; 2000 BP.

XX

AC ADJ41087;

XX

DT 06-MAY-2004 (first entry)

XX

DE Plant cDNA #2087.

XX

KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.

XX

OS Eukaryota.

XX

PN US2004016025-A1.

XX

PD 22-JAN-2004.

XX

PF 26-SEP-2002; 2002US-00260238.

XX

PR 26-SEP-2001; 2001US-0325277P.

XX

PR 26-SEP-2001; 2001US-0325448P.

XX

PR 04-APR-2002; 2002US-0370620P.

XX

PA (BUDW/) BUDWORTH P.

XX

PA (MOUG/) MOUGHAMER T.

XX

PA (BRIG/) BRIGGS S P.

XX

PA (COOP/) COOPER B.

XX

PA (GLAZ/) GLAZEBROOK J.

XX

PA (GOFF/) GOFF S A.

XX

PA (KATA/) KATAGIRI F.

XX

PA (KREP/) KREPS J.

XX

PA (PROV/) PROVART N.

XX

PA (RICK/) RICKE D.

XX

PA (ZHUT/) ZHU T.

XX

XX

PI Budworth P, Moughamer T, Briggs SP, Provart N, Ricke D, Zhu T;
 PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
 XX WPI; 2004-190374/18.
 DR
 XX New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 XX
 PS Claim 60; SEQ ID NO 2087; 230pp; English.

| | | | | |
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| FT | variation | /*tag= h | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(481,C) | | |
| FT | variation | /*tag= i | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(500,T) | | |
| FT | variation | /*tag= j | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(585,C) | | |
| FT | variation | /*tag= k | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(613,C) | | |
| FT | variation | /*tag= l | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(676,T) | | |
| FT | variation | /*tag= m | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(688..689,TGG) | | |
| FT | variation | /*tag= n | /*standard_name= | "Single nucleotide polymorphism" |
| FT | | replace(722,G) | | |
| FT | variation | | | |

| | | |
|----|-------------------------------|--|
| FT | variation | /standard_name replace(749,G, /tag= p /standard_name replace(754,C, /tag= q /standard_name |
| PT | | |
| FT | | |
| FT | | |
| FT | | |
| PT | variation | |
| FT | | |
| PT | | |
| FT | | |
| PT | | |
| XX | | |
| PN | WO2003104491-A1. | |
| PN | | |
| XX | | |
| PD | 18-DEC-2003. | |
| XX | | |
| XX | | |
| DE | 10-JUN-2003: 2003WO-JP007332. | |

10-JUN-2002; 2002JP-00168875.
(PLAN-) PLANT GENOME CENT CO LTD.
(NAAG-) NAT AGRIC RES ORG JAPAN.
Minobe Y, Monna L, Suzuki J, Ohta R, Nemoto H, Ideta O;
WPI; 2004-053624/05.
Distinguishing rice varieties based on polymorphism sites as markers to
show different patterns in combination, useful in distinguishing and
specifying varieties for quality control.
Claim 1: SEQ ID NO 22: 193bp; Japanese.

XX This invention relates to a novel method of distinguishing rice varieties
CC which comprises judging base types at any of 28 sites selected from the
CC rice genome, or of the bases in these sites of base pairs of the bases at
CC such sites in the complementary strand and relating the judged base types
CC with the rice variety. The method is useful in distinguishing and
CC specifying varieties analogous to each other at DNA level for quality
CC control of 24 rice varieties, to detect adulterants and mixing with
CC cheaper varieties for protection of small traders and consumers.
XX
XX Sequence 900 bp. 293 A. 161 C. 142 G. 304 T. 0 U. 0 Other:

| | Query Match | 4.7%; | Score 83.2; | DB 12; | Length 900; |
|----|-----------------------|---|--------------------|----------------|-------------|
| | Best Local Similarity | 87.9%; | Pred. No. 1.3e-11; | | |
| | Matches 102; | Conservative | 0; | Mismatches 13; | Indels 1; |
| | Gaps | | | | |
| QY | 1 | ACTTTAGATATAAAGTAAGTCACAGAGAAAAATAAATAATATTC-AAAATTTTTTAAAT | 59 | | |
| DB | 119 | ACTCTGGATATAAAGTAAAGTCACAATAAAATAAATAATATTCAAAATTTTCTGAAT | 178 | | |
| QY | 60 | AAGACGAGTGGTCAAACAGTCAACAGTAAAAAATCTCAAAAATCCTTATATATTGGGAC | 115 | | |
| DB | 179 | AAGACGAAATGGTCAAACAGTGCACAGTAAAAATGTCAAAAATCCCTTATATTAAAGGCAC | 234 | | |

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX WO2003000898-A1.
PN
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-IB001105.
PF
XX 22-JUN-2001; 2001WO-IB001105.
PR
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
PI
XX WPI; 2003-175290/17.
DR
XX
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
PT
XX Claim 27; SEQ ID NO 4820; 899pp; English.
PS
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to that
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 713 A; 326 C; 345 G; 616 T; 0 U; 0 Other;
Query Match 4.6%; Score 81.6; DB 8; Length 2000;
Best Local Similarity 87.1%; Pred. No. 5.1e-11;
Matches 101; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 1 ACTTTAGATAATAAGTAAAGTCACAGAAATAATAATAATCC-AAATTTTTTAAAT 59
DB 423 ACTGTGGATATAAAGTAAAGTCACAAATCAATAATAATAATTTCAAAATTTTGAAT 482
QY 60 AAGACGAGTGGTCAACAGTCAAGTAAACCTCAAAATTCCTTATATATCGGAC 115
DB 483 AAGACGAGTGGTCAACAGTCAAGTAAACCTCAAAATTCCTTATATATCGGAC 538
Search completed: November 17, 2004, 11:07:15
Job time : 830 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 10:46:50 ; Search time 174 Seconds
(without alignments)
7238.609 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 acttagataataagaag.....ctctctctcttcagtgcaag 1772

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | ID | Description |
|------------|-------|---------|--------------|----|---------------------|
| C 1 | 47.2 | 2.7 | 7218 | 1 | US-08-232-463-14 |
| C 2 | 45.6 | 2.6 | 640881 | 4 | US-09-790-988-1 |
| C 3 | 43 | 2.4 | 832 | 4 | US-09-621-976-2813 |
| 4 | 42.8 | 2.4 | 1141 | 4 | US-09-806-708B-22 |
| 5 | 42 | 2.4 | 3602 | 4 | US-09-402-929-1 |
| 6 | 40.2 | 2.3 | 640681 | 4 | US-09-790-988-1 |
| 7 | 39 | 2.2 | 3738 | 4 | US-09-710-279-3978 |
| 8 | 39 | 2.2 | 3926 | 4 | US-09-710-279-4015 |
| 9 | 38.6 | 2.2 | 8607 | 4 | US-10-204-708-71 |
| 10 | 38.4 | 2.2 | 450 | 4 | US-09-270-767-12394 |
| 11 | 38.4 | 2.2 | 81001 | 4 | US-09-750-580-1 |
| 12 | 38.2 | 2.2 | 195 | 4 | US-09-270-767-8025 |
| 13 | 38.2 | 2.2 | 1141 | 4 | US-09-270-767-23307 |
| 14 | 38.2 | 2.2 | 1242 | 4 | US-09-806-708B-22 |
| 15 | 38 | 2.1 | 3758 | 3 | US-09-248-796A-352 |
| 16 | 37.8 | 2.1 | 4383 | 3 | US-08-323-477-1 |
| 17 | 37.8 | 2.1 | 4383 | 3 | US-08-397-653B-2 |
| 18 | 37.8 | 2.1 | 4383 | 6 | 5175095-4 |
| 19 | 37.8 | 2.1 | 4383 | 6 | 5177307-1 |
| C 20 | 37.8 | 2.1 | 6070 | 4 | US-10-204-708-10 |
| C 21 | 37.6 | 2.1 | 1017 | 4 | US-09-710-279-1003 |
| C 22 | 37.6 | 2.1 | 1092 | 3 | US-09-134-001C-1876 |
| 23 | 37.6 | 2.1 | 2031 | 3 | US-09-693-147-5 |
| 24 | 37.6 | 2.1 | 2781 | 3 | US-08-749-522-4 |
| 25 | 37.6 | 2.1 | 3285 | 4 | US-09-710-279-4141 |
| 26 | 37.6 | 2.1 | 1131 | 4 | US-10-204-708-28 |
| 27 | 37.4 | 2.1 | 3126 | 4 | US-09-710-279-3912 |

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| 28 | 37.4 | 2.1 | 5735 | 4 | US-09-734-674-1 |
| 29 | 37.4 | 2.1 | 11015 | 4 | US-10-204-708-55 |
| C 30 | 37.4 | 2.1 | 202001 | 4 | US-09-734-674-3 |
| 31 | 37.4 | 2.1 | 1664976 | 4 | US-08-916-421B-1 |
| 32 | 37.4 | 2.1 | 1664976 | 4 | US-09-692-570-1 |
| 33 | 37 | 2.1 | 786431 | 4 | US-09-751-389-3 |
| C 34 | 36.8 | 2.1 | 505 | 4 | US-09-621-976-15639 |
| 35 | 36.8 | 2.1 | 691 | 4 | US-09-270-767-29557 |
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| 37 | 36.8 | 2.1 | 5392 | 4 | US-08-880-066-5 |
| 38 | 36.4 | 2.1 | 359 | 4 | US-03-270-767-3877 |
| 39 | 36.4 | 2.1 | 359 | 4 | US-09-270-767-19159 |
| 40 | 36.4 | 2.1 | 365 | 4 | US-09-621-976-16042 |
| 41 | 36.4 | 2.1 | 371 | 4 | US-09-621-976-16048 |
| C 42 | 36.4 | 2.1 | 881 | 4 | US-08-956-171E-518 |
| C 43 | 36.4 | 2.1 | 881 | 4 | US-08-781-986A-518 |
| C 44 | 36.4 | 2.1 | 1055 | 4 | US-09-806-708B-23 |
| C 45 | 36.4 | 2.1 | 6317 | 4 | US-10-204-708-11 |

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match

2.7%; Score 47.2; DB 1; Length 7218;


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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1) (1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEL promoters
US-09-806-708B-22

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Query Match      2.4%; Score 42.8; DB 4; Length 1141;
Best Local Similarity 9.9%; Pred. No. 0.038;
Matches 56; Conservative 238; Mismatches 267; Indels 3; Gaps 2;

QY 212 ATGAGAGTCGCGAGTACGAGTACCTACCACTGCTTCTTCACTGAGCTAGCTG 271
Db 149 WTTCMCMDDKDKRTRWKKNNATGDDDDTKYHMMNNNGCBVTWVRYKTDSDSBR 208
QY 272 CATGTTCTGCTGCAATTCATTCGAGGAGCAGCTAGCAAGTTCGAGGAAACAATC 331
Db 209 MNYGBWKNWSDVYTYVWVWMDMCKRYRVRTRGRMRYWVWABTAHRRRYNNGWT 268
QY 332 GATAATCCATTGTCGAGGAGGAACATCGAGAAACCGGGCTCGAGACGAGCGGAG 391
Db 269 BAAVRRWTHNNNNNAKAMCKRAKYGWNRABVNSTCTTWKSKITKVRTSCWANNCRAG 328
QY 392 CAGCTGTACCGTACGTTCTGAGGCTGAACCATCTCGCAATCCGAGATTGTTGCT 451
Db 329 DANKDHKM--WKWSAAMGVVNNNNNNNTYKKARHBAEWDVWHSWKKWHANAHAHYSR 386
QY 452 TCAATTCCAACTTGAGTCTCTCAGATTGCTGATGTTCAACCGTAGTACATCTGAAA 511
Db 387 KWTBYKRTMYNNNGITTMKRMWAWYWKMDMBEGTYNNNNNGRTYGYGWTGNKMMWT 446
QY 512 ATGA-AGTGTAAATACCTTGAGAAGACCTTCATGGAAGCAGCTCGAGCGGCAATTAGCT 570
Db 447 YVKKANCKKWAEDHKCTHNNNTWKKTYNNCYKSMNTNGKSHRBAABAVYTWYMMW 506
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RESULT 5
US-09-402-929-1
; Sequence 1, Application US/09402929
; Patent No. 6410825
; GENERAL INFORMATION:
; APPLICANT: Temple University - Of The Commonwealth System of Higher Education
; APPLICANT: Toscani, Antonio
; APPLICANT: Hatton, Kimi
; APPLICANT: Reddy, E. P.
; TITLE OF INVENTION: A-mvb NULL MUTANT TRANSGENIC ANIMALS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,929
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/06896
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-214 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3602 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-402-929-1

Query Match      2.4%; Score 42; DB 4; Length 3602;
Best Local Similarity 52.9%; Pred. No. 0.12;
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 3 TTATAGATAAAGTAAGTCAAGCAAGAAATAAATAAATTAATCCAAATTTTAAATAAG 62
Db 3433 TGTGTTTTAAAGTAGITTTAAATGTACTAAATAAATAAATTTCTTTTAAA 3492
QY 63 ACAGTGTGTCACACAGTCAAGTAAACCTCAAAATTCCTTATATATGCGGACTTATAT 122
Db 3493 TTATATGCGGGTCTATATAATTAATCTGCTGATGTTATGTTGTTGAATTTTCA 3552
QY 123 ATGGACGAGGAGGAGTAGAAGATTGTAGCCAGAGAAAAAACAACAAAAA 172
Db 3553 TTTGTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3602

```

```

RESULT 6
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

```

```

Query Match      2.3%; Score 40.2; DB 4; Length 640681;
Best Local Similarity 53.5%; Pred. No. 6.7;
Matches 84; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 640 AGTGATTTTCTACTATTGTCAGTTTAAACCGCTAATAGTACAGATATAAATTTTCTAT 699
Db 125520 AATAATAATATTATTTTAAAGTTTAAAGTAAATACTACAAAAAAATCTCGTAAAT 125579
QY 700 AGATCAATTAATAATCAATTTTATGTTCTGTTCAATTTTCTACCACTTATCAACATA 759

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/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12394
/ LENGTH: 450
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
US-09-270-767-12394

Query Match      2.2%; Score 38.6; DB 4; Length 450;
Best Local Similarity 51.4%; Pred. No. 0.37;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      6 AGATAATAAGTAAGTCACAGAAATAAATAATTCCTTATATATGGACTTATATTG 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 AGACATGTCAGAAACCAAGATAAATAATTCCTTATATATTAATTTAAATTATA 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      66 AGTGGTCAACAGTACAGTCAAGTCAAACTCAAAATTCCTTATATATGGACTTATATTG 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61 TAATGTAAATCAACACACACAAATTCCTTATATTAATTTAAATTATAATTATA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      126 GGACGAGGAAGTAGAAGATTGTAGCAAGAAAGAAAAACAAACACACACC 178
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      121 ATAAATATAAAATAAATAAACAATAAATAATTCAAAAAACAACAAATAACC 173
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-09-750-580-1/c
/ Sequence 1, Application US/09750580
/ Patent No. 6455280
/ GENERAL INFORMATION:
/ APPLICANT: Yen, Frances
/ APPLICANT: Denison, Blake
/ APPLICANT: Bour, Barbara
/ APPLICANT: Bihain, Bernard
/ APPLICANT: Dumas Milne Edwards, Jean-Baptiste
/ APPLICANT: Duclert, Aymeric
/ APPLICANT: Bougueleret, Lydie
/ APPLICANT: Ebbets-Reed, Dana
/ APPLICANT: Salter-Cid, Luisa
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
/ FILE REFERENCE: 89, US2.CIP
/ CURRENT APPLICATION NUMBER: US/09/750,580
/ CURRENT FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: US 09/599,362
/ PRIOR FILING DATE: 2000-06-21
/ PRIOR APPLICATION NUMBER: PCT/IB00/0101
/ PRIOR FILING DATE: 2000-06-21
/ PRIOR APPLICATION NUMBER: PCT/IB99/02058
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: US 49/469/099
/ PRIOR FILING DATE: 1999-12-21
/ PRIOR APPLICATION NUMBER: US 60/113,686
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: US 60/141,032
/ PRIOR FILING DATE: 1999-06-25
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 81001
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: 10946..12946
/ OTHER INFORMATION: 5'regulatory region
/ NAME/KEY: exon
/ LOCATION: 12947..12958
/ OTHER INFORMATION: exon 1
/ NAME/KEY: exon
/ LOCATION: 13470..13526
/ OTHER INFORMATION: exon 2
/ NAME/KEY: exon
/ LOCATION: 12348..12366
```

```
/ LOCATION: 13641..13752
/ OTHER INFORMATION: exon 3
/ NAME/KEY: exon
/ LOCATION: 14271..15968
/ OTHER INFORMATION: exon 4
/ NAME/KEY: misc.feature
/ LOCATION: 15969..17969
/ OTHER INFORMATION: 3'regulatory region
/ NAME/KEY: allele
/ LOCATION: 1239
/ OTHER INFORMATION: 20-828-311 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 12347
/ OTHER INFORMATION: 17-42-319 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 15241
/ OTHER INFORMATION: 17-41-250 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 42218
/ OTHER INFORMATION: 20-841-149 : polymorphic base A or G
/ NAME/KEY: allele
/ LOCATION: 45442
/ OTHER INFORMATION: 20-842-115 : polymorphic base A or G
/ NAME/KEY: allele
/ LOCATION: 77058
/ OTHER INFORMATION: 20-853-415 : polymorphic base C or T
/ NAME/KEY: primer bind
/ LOCATION: 929..949
/ OTHER INFORMATION: 20-828.pu
/ NAME/KEY: primer bind
/ LOCATION: 1357..1377
/ OTHER INFORMATION: 20-828.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 12029..12050
/ OTHER INFORMATION: 17-42.pu
/ NAME/KEY: primer bind
/ LOCATION: 12581..12603
/ OTHER INFORMATION: 17-42.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 14992..15012
/ OTHER INFORMATION: 17-41.pu
/ NAME/KEY: primer bind
/ LOCATION: 15460..15482
/ OTHER INFORMATION: 17-41.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 42070..42090
/ OTHER INFORMATION: 20-841.pu
/ NAME/KEY: primer bind
/ LOCATION: 42572..42591
/ OTHER INFORMATION: 20-841.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 45328..45347
/ OTHER INFORMATION: 20-842.pu
/ NAME/KEY: primer bind
/ LOCATION: 45863..45883
/ OTHER INFORMATION: 20-842.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 76644..76664
/ OTHER INFORMATION: 20-853.pu
/ NAME/KEY: primer bind
/ LOCATION: 77166..77185
/ OTHER INFORMATION: 20-853.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 1220..1238
/ OTHER INFORMATION: 20-828-311.mis
/ NAME/KEY: primer bind
/ LOCATION: 1240..1258
/ OTHER INFORMATION: 20-828-311.mis complement
/ NAME/KEY: primer bind
/ LOCATION: 12328..12346
/ OTHER INFORMATION: 17-42-319.mis
/ NAME/KEY: primer bind
/ LOCATION: 12348..12366
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OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42205..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match      2.2%; Score 38.4; DB 4; Length 81001;
Best Local Similarity 50.5%; Pred. No. 7.2;
Matches 93; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 10 AATAAGTAGTCACAAGAAAATAAATAATCCAAATTTTAAATAGCAGGTG 69
Db 52930 AAGCAAGGGTGACAAGAGGAAATAGAGAGAAATCTAGGATAAAATCAGAACAGAGT 52871

Qy 70 GTCAACAGTACAAGTAAATACTCAAAATTCCTTATATATGGGACTTATATATGGAC 129
Db 52870 GGAATAAGCACTGAGAGAAATAGACAAATTAATAGTAAATAAACTAGGTCA 52811

Qy 130 GGAGGAAGTAGAAGATTGTAGCCAGAGAAAACAAAACACACACCGCCACTGGCA 189
Db 52810 GGGAGAATTCCTAAGTTTGGGTCCCAAAATTTAAAAACAAAAAACTCGGTAGCA 52751

Qy 190 GGCA 193
Db 52750 GGGA 52747

RESULT 12
US-09-767-8025
; Sequence 8025, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8025
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8025
Query Match      2.2%; Score 38.2; DB 4; Length 195;
Best Local Similarity 52.1%; Pred. No. 0.31;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAAGTCACAAGAAAATAAATAATTCCAAATTTTAAATAGACGA 66
Db 33 GATCAGTAAACACATCACAAAAAAGAACTCAGTCTCACATAATTTGGGGCTCAACA 92

Qy 67 GTGTCACACAGTACAGTAAATACTCAAAATTCCTTATATATGGGACTTATATATGG 126
Db 93 ATTAATATACACAAAATTAACCAAAATACAGAGTGTAAAGGTAGTAACAGTGTGA 152

Qy 127 GACGGAGGAAGTAGAGATTGTAGCCAAAGAAAAACAAAAAC 169
Db 153 AAAACAAGATTAAATATATATGAAAAAAGAAAAAAGAAAAAC 195

RESULT 13
US-09-270-767-23307
; Sequence 23307, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 23307
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23307
Query Match      2.2%; Score 38.2; DB 4; Length 195;
Best Local Similarity 52.1%; Pred. No. 0.31;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAAGTCACAAGAAAATAAATAATTCCAAATTTTAAATAGACGA 66
Db 33 GATCAGTAAACACATCACAAAAAAGAACTCAGTCTCACATAATTTGGGGCTCAACA 92

Qy 67 GTGTCACACAGTACAGTAAATACTCAAAATTCCTTATATATGGGACTTATATATGG 126
Db 93 ATTAATATACACAAAATTAACCAAAATACAGAGTGTAAAGGTAGTAACAGTGTGA 152

Qy 127 GACGGAGGAAGTAGAGATTGTAGCCAAAGAAAAACAAAAAC 169
Db 153 AAAACAAGATTAAATATATATGAAAAAAGAAAAAAGAAAAAC 195

RESULT 14
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03

```


QY 250 TGCTTCTTCAAGTACGCTAGCTGATGTTCTGTTCTGCTATTACATTGCGAGCAGCAGCTA 309
|||
Db 127 TG-TTCTTCAAGTACCAAGTGCATGTTCTGTTCTGCTATTGCAATTCGACGACGAGCTA 69
|||
QY 310 GCACAGTTTGCAGGACAAATCGATAATCCATTGTCGAGGAGGAAACATCGAGAAAAC 369
|||
Db 68 GCGACAGTTTGCAGGAGCTGTCGATCATCCAGTGTGTCACGTAGAGACATGCAATGAAAGC 9
|||
QY 370 CGGGGCTG 377
|||
Db 8 CCGGGCTG 1
|||

RESULT 2

US-10-260-238-1841
; Sequence 1841, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1841
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: {661}..(661)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: {683}..(683)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: {749}..(749)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1841

Query Match 5.0%; Score 87.8; DB 16; Length 2000;
Best Local Similarity 85.2%; Pred. No. 2.4e-11;
Matches 98; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 ACTTTAGATAATAAGTAAAGTACCAAGAAATAATAATAATATTCCTTATATTTTAAATA 60
|||
Db 1825 ACTTTGGATAATAAAGCAAGTACCAATAATAATAATAATAATTCCTTATATTTTAAATA 1884
|||
QY 61 AGACGAGTGGTCAACAGTACAGTAAACCTCAAAATTCCTTATATTTTGGGAC 115
|||
Db 1885 AGACGAATGATAAAACAGTATATACAAATGTCAAAATCCCTTATATTTAGAGGAC 1939
|||

RESULT 3

US-10-168-273B-1

; Sequence 1, Application US/10168273B
; Publication No. US20040058324A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Yamanouchi, Utako
; TITLE OF INVENTION: PLANT LESION FORMATION SUPPRESSING GENE, Sp17 AND USE THEREOF
; FILE REFERENCE: 23572-005 NATL
; CURRENT APPLICATION NUMBER: US/10/168,273B
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/JP01/09153
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: JP 2000-318557
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5579
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: genomic DNA
; NAME/KEY: CDS
; LOCATION: {3711}..(3947)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {4185}..(5327)
US-10-168-273B-1

Query Match 4.8%; Score 85.8; DB 16; Length 5579;
Best Local Similarity 88.2%; Pred. No. 1.3e-10;
Matches 105; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

QY 1 ACTTTAGATAATAAGTAAAGTACCAAGAAATAATAATAATATTCCTTATATTTTAAATA 60
|||
Db 2257 ACTTTAGATAATAAAGTAAGT--CAAAAAGAGATAATAATAATTTTAAATTTTAAATA 2314
|||
QY 61 AGACGAGTGGTCAACAGTACAGTAAACCTCAAAATTCCTTATATTTTGGGACTTAT 119
|||
Db 2315 AGACGATTGGTCAACAGTGCNAATTAATAACTCAAGATCCCTTATATTTATGGATAAAT 2373
|||

RESULT 4

US-10-260-238-2087/c
; Sequence 2087, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2087
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa

FEATURE:
NAME/KEY: N region
LOCATION: (433)..(433)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: N region
LOCATION: (1346)..(1346)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: N region
LOCATION: (1355)..(1355)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: N region
LOCATION: (1386)..(1386)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: N region
LOCATION: (1394)..(1394)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: N region
LOCATION: (1402)..(1402)
OTHER INFORMATION: n = any nucleotide
US-10-260-238-2087

Query Match 4.8%; Score 84.2; DB 16; Length 2000;
Best Local Similarity 88.0%; Pred. No. 2e-10;
Matches 103; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 3 TTTAGATAATAAGTAAGTACAGCAAGAAAATAATAATAATTCACAAATTTTTTTAATAAG 62
DB 344 TTGGGATAATAAGTAAGTACAGCAAGAAAATAATAATAATTCACAAATTTTTTTAATAAG 286
QY 63 ACAGTGGTCAACAGTACAGTAAACAAATTCCTATATATATGGGACTTAT 119
DB 285 ATGAGTGGTCAACAGTGGCAAGCAAAACTCAAAATCCCTATATATATGGGCGGAT 229

RESULT 5
US-09-840-743-19/c
Sequence 19, Application US/09840743
Publication No. US20030135890A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Choi, Yoonhee
APPLICANT: Hannon, Mike
APPLICANT: Okamura, Jack Kishiro
APPLICANT: Tatarinova, Tatiana Valerievna
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-099910US
CURRENT APPLICATION NUMBER: US/09/840,743
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 09/553,690
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 12120
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: DMTRICE sequence from PAC P0489GG09
US-09-840-743-19

Query Match 4.5%; Score 80.4; DB 10; Length 12120;
Best Local Similarity 73.4%; Pred. No. 4.6e-09;
Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
QY 1 ACTTTAGATAATAAGTAAGTACAGCAAGAAAATAATAATAATTCACAAATTTTTTTAAT 59
DB 11342 ACTGTGAATAATAAGTAAGTACAGCAAGAAAATAATAATAATTCACAAATTTTTTTAAT 11283

QY 60 AAGACGAGTGGTCAACAGTACAAAGTAAATACTCAAAATTCCTATATATGGGACTTAT 119
DB 11282 AAGCGAGTGGTCAACAGTTCGAAGCAAAACTCAAAATCTCTTATATTTGGGACGGAG 11223
QY 120 ATTATGGACGGAGGAAGTAGAAGATTGTAGCCAGAA 157
DB 11222 GGAGTAGCAATTTCTACCCCTAAGCAGCTTTCTGCCAACAA 11185

RESULT 6
US-10-260-238-2150
Sequence 2150, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiya
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2150
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza sativa
US-10-260-238-2150

Query Match 4.5%; Score 80; DB 16; Length 2000;
Best Local Similarity 86.2%; Pred. No. 2.3e-09;
Matches 100; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
QY 1 ACTTTAGATAATAAGTAAGTACAGCAAGAAAATAATAATAATTCACAAATTTTTTTAAT 59
DB 352 ACGGTAGATAATAAGTAAGTACAAATAATAATAATAATTCACAAATTTTTTTAAT 411
QY 60 AAGACGAGTGGTCAACAGTACAAAGTAAATACTCAAAATTCCTATATATGGGAC 115
DB 412 AAGACGAGTGGTCAAAATTTGCAACAAATAATCCCTATATATATGGGAC 467

RESULT 7
US-10-260-238-2454
Sequence 2454, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiya
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

QY 60 AAGACGAGTGGTCAAAACAGTACAAGTAAAACTCAAAATTCCTTATATTATGGGAC 115
 |||
 Db 1507 AAGACGAGTGGTCAAAACGTTGCAAGCAAAATCTTATAATCCCTTATATTATGGGAC 1452
 |||

RESULT 9
 US-10-260-238-1664/c
 ; Sequence 1664, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiya
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1664
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-260-238-1664

Query Match 4.3%; Score 76.8; DB 16; Length 2000;
 Best Local Similarity 84.5%; Pred. No. 1.5e-08;
 Matches 98; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 ACTTTAGATATATAAAGTAACTCACAAGAAAAATAATAATAATTCCAAATTTTTT-AAAT 59
 |||
 Db 1161 ACTGTGGATATAAAGTAAAGTCACAATATAATAATAATAATTTTAAAAAAATTAAT 1102
 |||

QY 60 AAGACGAGTGGTCAAAACAGTACAAGTAAAACTCAAAATTCCTTATATTATGGGAC 115
 |||
 Db 1101 AAGACGAGTATCAACATGTGAAGCAAAACACAAAATTCCTTATATTATGGGAC 1046
 |||

RESULT 10
 US-10-437-963-10006
 ; Sequence 10006, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 10006
 ; LENGTH: 6064

; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16369C.1
US-10-437-963-1006

Query Match 4.2%; Score 75; DB 17; Length 6064;
Best Local Similarity 88.9%; Pred. No. 7.5e-08;
Matches 104; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 1 ACTTTAGATATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGGGAC 58
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Db 3210 ACTTTGATATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGGGAC 3268
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QY 59 TAAGACGAGTGGTCAACAGTACAGTAAAGTCAAAATTCCTTATATGGGAC 115
|||||
Db 3269 TAAGACGAGTAAATCAAGAGTCAAGTCAAAATTCCTTATATGGGAC 3325
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RESULT 11
US-10-260-238-2176
; Sequence 2176, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricks, Bartell
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2176

; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (573)..(573)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (600)..(600)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1711)..(1711)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1929)..(1929)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1941)..(1941)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1960)..(1960)

; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1968)..(1968)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1991)..(1991)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1994)..(1994)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1999)..(1999)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-2176

Query Match 4.2%; Score 73.8; DB 16; Length 2000;
Best Local Similarity 84.1%; Pred. No. 8.5e-08;
Matches 95; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1 ACTTTAGATATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGG 112
|||||
Db 1551 ACCGTAGATAATAAGTAAGTCACTCAAAATAATAATAATTCCTTATATGG 1610
|||||
QY 60 AAGACGAGTGGTCAACAGTACAGTAAAGTCAAAATTCCTTATATGG 112
|||||
Db 1611 AATACGAGTATCAACAGTGTGAAGTAAAGTCAAAATTCCTTATATGG 1663
|||||

RESULT 12
US-10-437-963-50400/c
; Sequence 50400, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 50400
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52890C.1
US-10-437-963-50400

Query Match 4.1%; Score 73.4; DB 17; Length 5216;
Best Local Similarity 84.7%; Pred. No. 1.8e-07;
Matches 94; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
QY 1 ACTTTAGATATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGG 59
|||||
Db 5074 ACTTTAGATATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGG 5015
|||||
QY 60 AAGACGAGTGGTCAACAGTACAGTAAAGTCAAAATTCCTTATATGG 110
|||||
Db 5014 AAGACAGTGTCTCAACAGTGTCAAGTCAAAATTCCTTATATGG 4964
|||||

RESULT 13

Thu Nov 18 13:23:03 2004

US-10-260-238-1731/c
 ; Sequence 1731, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd R.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-1P
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1731
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; US-10-260-238-1731

Query Match 4.1%; Score 72.8; DB 16; Length 2000;
 Best Local Similarity 80.8%; Pred. No. 1.5e-07;
 Matches 97; Conservative 0; Mismatches 22; Indels 1; Gaps 1;
 QY 1 ACTTTAGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 60
 DB 1119 ACTTTGGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 1061
 QY 61 AGACGAGTGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGGGACTTATA 120
 DB 1060 AGACGAGTGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGAACGGAGA 1001

RESULT 14
 US-10-437-963-34025/c
 ; Sequence 34025, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 34025
 ; LENGTH: 2955
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; US-10-437-963-34025

Query Match 3.9%; Score 69; DB 17; Length 1480;
 Best Local Similarity 85.5%; Pred. No. 1.2e-06;
 Matches 100; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
 QY 1 ACTTTAGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 59
 DB 1287 ATTTTAGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 1228
 QY 60 AAGACGAGT-GGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGGGAC 115
 DB 1227 AAGACGAGTGGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGAGAC 1171

Search completed: November 17, 2004, 16:37:15
 Job time : 903 secs

US-10-260-238-1731/c
 ; Sequence 1731, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd R.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-1P
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1731
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; US-10-260-238-1731

Query Match 4.1%; Score 72.2; DB 17; Length 2955;
 Best Local Similarity 80.8%; Pred. No. 1.5e-07;
 Matches 97; Conservative 0; Mismatches 22; Indels 1; Gaps 1;
 QY 1 ACTTTAGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 60
 DB 1119 ACTTTGGATAATAAGTAAAGTACACAGAAATAATAATAATTCCTTATTTTGAATA 1061
 QY 61 AGACGAGTGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGGGACTTATA 120
 DB 1060 AGACGAGTGGTCAACAGTACAAAGTAAACCTCAAAATTCCTTATTTATGAACGGAGA 1001

RESULT 14
 US-10-437-963-34025/c
 ; Sequence 34025, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 34025
 ; LENGTH: 2955
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; US-10-437-963-34025

Query Match 4.1%; Score 72.2; DB 17; Length 2955;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 10:45:20 ; Search time 5094. Seconds
(without alignments)
12675.933 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actcttagataataaagtaag.....ctcttctcttcagtgcaag 1772

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| C 1 | 460.6 | 26.0 | 493 | AB157032 | Oryza sat |
| C 2 | 148.2 | 8.4 | 626 | CL552633 | OB_Ba009 |
| C 3 | 131.4 | 7.4 | 802 | CL549942 | OB_Ba008 |
| C 4 | 99 | 5.6 | 609 | CL709985 | OR_BBa003 |
| C 5 | 98.2 | 5.5 | 663 | AQ872280 | nbeb0047D |
| C 6 | 97.2 | 5.4 | 783 | CL734947 | OR_BBa006 |
| C 7 | 95.8 | 5.4 | 681 | CL837854 | OR_CBa006 |
| C 8 | 92.6 | 5.2 | 406 | CL712255 | OR_BBa003 |
| C 9 | 92.6 | 5.2 | 641 | CL625050 | OR_BBa002 |
| C 10 | 91 | 5.1 | 703 | CL725327 | OR_BBa005 |
| C 11 | 90.4 | 5.1 | 582 | CL788096 | OR_BBa010 |
| C 12 | 90.4 | 5.1 | 660 | CL826141 | OR_CBa004 |
| C 13 | 90.2 | 5.1 | 764 | CL795980 | OR_CBa000 |
| C 14 | 89.4 | 5.0 | 881 | CL732636 | OR_BBa006 |
| C 15 | 88 | 5.0 | 566 | CL617540 | OR_BBa001 |
| C 16 | 88 | 5.0 | 569 | AQ272200 | nbbx0027L |
| C 17 | 88 | 5.0 | 643 | CL770798 | OR_BBa014 |
| C 18 | 88 | 5.0 | 767 | CL732306 | OR_BBa006 |
| C 19 | 87.8 | 5.0 | 375 | CL782567 | OR_BBa009 |
| C 20 | 87.8 | 5.0 | 482 | CL520455 | OR_BBa007 |
| C 21 | 87.8 | 5.0 | 573 | CL743078 | OR_BBa007 |
| C 22 | 87.8 | 5.0 | 820 | AQ861700 | nbeb0017G |
| C 23 | 87 | 4.9 | 478 | CL733727 | OR_BBa006 |
| C 24 | 87 | 4.9 | 680 | AQ289268 | nbbx0034B |

| | | | | | | |
|------|------|-----|-----|---|----------|-----------|
| C 25 | 86.8 | 4.9 | 606 | 9 | CL744089 | OR_BBa008 |
| C 26 | 86.8 | 4.9 | 679 | 9 | CL756822 | OR_BBa012 |
| C 27 | 86.4 | 4.9 | 711 | 9 | CL764853 | OR_BBa013 |
| C 28 | 86.4 | 4.9 | 835 | 9 | CL776676 | OR_BBa009 |
| C 29 | 86.2 | 4.9 | 536 | 9 | CL733616 | OR_BBa006 |
| C 30 | 86.2 | 4.9 | 703 | 9 | CL782409 | OR_BBa009 |
| C 31 | 86.2 | 4.9 | 728 | 6 | CB663138 | OSJNED07M |
| C 32 | 86.2 | 4.9 | 744 | 9 | CL755341 | OR_BBa012 |
| C 33 | 86.2 | 4.9 | 822 | 9 | CL755195 | OR_BBa012 |
| C 34 | 85.8 | 4.8 | 744 | 9 | CL817420 | OR_CBa003 |
| C 35 | 84.8 | 4.8 | 429 | 8 | AQ509735 | OR_BBa003 |
| C 36 | 84.8 | 4.8 | 512 | 9 | CL710177 | OR_BBa003 |
| C 37 | 84.8 | 4.8 | 528 | 9 | CL746902 | OR_BBa011 |
| C 38 | 84.8 | 4.8 | 556 | 8 | AQ509717 | nbxb0096H |
| C 39 | 84.8 | 4.8 | 633 | 8 | AQ510370 | nbxb0095G |
| C 40 | 84.8 | 4.8 | 879 | 9 | CL762853 | OR_BBa013 |
| C 41 | 84.6 | 4.8 | 628 | 8 | AQ157226 | nbxb0009K |
| C 42 | 84.2 | 4.8 | 696 | 9 | CL715023 | OR_BBa003 |
| C 43 | 83.8 | 4.7 | 588 | 9 | CL717546 | OR_BBa004 |
| C 44 | 83.8 | 4.7 | 700 | 9 | CL841972 | OR_CBa007 |
| C 45 | 83.8 | 4.7 | 715 | 9 | CL827638 | OR_CBa004 |

ALIGNMENTS

AB157032 493 bp DNA linear GSS 23-DEC-2003
Oryza sativa (japonica cultivar-group) DNA, clone:T27150T, 3',
flanking sequence of Tos1 insertion in rice strain NG0531, genomic
survey sequence.

AB157032

AB157032.1 GI:40315745

GSS.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales;

Eurhartoideae; Oryzaeae; Oryza.

1

Miyao, A., Tanaka, K., Murata, K., Sawaki, H., Takeda, S., Abe, K.,

Shinozuka, Y., Onosato, K. and Hirochika, H.

Target site specificity of the Tos1 retrotransposon shows a

preference for insertion within genes and against insertion in

retrotransposon-rich regions of the genome

Plant Cell 15 (8), 1771-1780 (2003)

12897251

2 (bases 1 to 493)

Miyao, A. and Hirochika, H.

Direct Submission

Submitted (19-DEC-2003) Akio Miyao, National Institute of

Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,

Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,

URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,

Fax:81-298-38-7020)

Location/Qualifiers

1. 493

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/strain="NG0531"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="T27150T"

/clone_lib="PCR product directly amplified from rice

genomic DNA"

/note="The 3' end of retrotransposon Tos1.7 was found

immediately upstream of this sequence."

ORIGIN

Query Match 26.0%; Score 460.6; DB 9; Length 493;

Best Local Similarity 98.4%; Pred. No. 3.5e-105;

Matches 485; Conservative 0; Mismatches 6; Indels 2; Gaps 2;


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FEATURES
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    Location/Qualifiers
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        /organism="Oryza sativa (Japonica cultivar-group)"
        /mol_type="genomic DNA"
        /cultivar="Nipponbare"
        /db_xref="taxon:39947"
        /clone="nbeb0047D09r"
        /tissue_type="Leaf"
        /lab_host="E. coli DH10B"
        /clone_lib="CUGI Rice BAC Library (EcoRI)"
        /notes="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
```

Query Match 5.5%; Score 98.2; DB 8; Length 663;
 Best Local Similarity 89.1%; Pred. No. 1.5e-13;
 Matches 106; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 1 ACTTTAGATTAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 60
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Qy 61 AGACGAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 119
Db 260 AGACAAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 318

RESULT 6
CL734947 783 bp DNA linear GSS 27-JUL-2004
LOCUS OR_BBa0068F07.f OR_BBa Oryza rufipogon genomic clone OR_BBa0068F07
DEFINITION 5', genomic survey sequence.
ACCESSION CL734947
VERSION CL734947.1 GI:50669303
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 783)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0063 row: G column: 17
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
  1..681
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    /mol_type="genomic DNA"
    /db_xref="taxon:4529"
    /clone="OR_CBa0063G17"
    /tissue_type="young leaves"
    /dev_stage="2 week old seedlings"
    /lab_host="DH10B T1 phage resistant"
    /clone_lib="OR_CBa"
    /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

FEATURES
  source
    Location/Qualifiers
      1..681
        /organism="Oryza rufipogon"
        /mol_type="genomic DNA"
        /db_xref="taxon:4529"
        /clone="OR_CBa0063G17"
        /tissue_type="young leaves"
        /dev_stage="2 week old seedlings"
        /lab_host="DH10B T1 phage resistant"
        /clone_lib="OR_CBa"
        /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

FEATURES
  source
    Location/Qualifiers
      1..783
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        /lab_host="DH10B-T1 phage resistant"
        /clone_lib="OR_BBa"
        /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

ORIGIN
  Query Match 5.5%; Score 97.2; DB 9; Length 783;
  Best Local Similarity 89.0%; Pred. No. 2.7e-13;
  Matches 105; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ACTTTAGATTAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 60
Db 321 ACTTTGGATTAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 380
Qy 61 AGACGAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 118
Db 381 AGACAAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGAATTGA 438

RESULT 7
CL837854 681 bp DNA linear GSS 09-AUG-2004
LOCUS OR_CBa0063G17.r OR_CBa Oryza rufipogon genomic clone OR_CBa0063G17
DEFINITION 3', genomic survey sequence.
ACCESSION CL837854
VERSION CL837854.1 GI:51083464
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 681)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0063 row: G column: 17
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:4529"
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    /tissue_type="young leaves"
    /dev_stage="2 week old seedlings"
    /lab_host="DH10B T1 phage resistant"
    /clone_lib="OR_CBa"
    /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

FEATURES
  source
    Location/Qualifiers
      1..681
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        /db_xref="taxon:4529"
        /clone="OR_CBa0063G17"
        /tissue_type="young leaves"
        /dev_stage="2 week old seedlings"
        /lab_host="DH10B T1 phage resistant"
        /clone_lib="OR_CBa"
        /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

FEATURES
  source
    Location/Qualifiers
      1..783
        /organism="Oryza rufipogon"
        /mol_type="genomic DNA"
        /db_xref="taxon:4529"
        /clone="OR_BBa0068F07"
        /tissue_type="young leaves"
        /lab_host="DH10B-T1 phage resistant"
        /clone_lib="OR_BBa"
        /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0068 row: F column: 07
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
  1..783
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    /db_xref="taxon:4529"
    /clone="OR_BBa0068F07"
    /tissue_type="young leaves"
    /lab_host="DH10B-T1 phage resistant"
    /clone_lib="OR_BBa"
    /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII;"

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TITLE      OMAP Project
JOURNAL    Unpublished (2004)
COMMENT    Contact: Rod A. Wing
           Arizona Genomics Institute
           University of Arizona
           Forbes Building Room 303, Tucson, AZ 85721-0036, USA
           Tel: 520 626 9595
           Fax: 520 621 1259
           Email: http://genome.arizona.edu
           PCR Primers
           FORWARD: TAA TAC GAC TCA CTA TAG GG
           BACKWARD: CAC TCA TTA GGC ACC CCA
           Insert Length: 161 Std Error: 0.00
           Plate: 0055 row: D column: 11
           Seq primer: TAA TAC GAC TCA CTA TAG GG
           Class: BAC ends.

FEATURES   Location/Qualifiers
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           /mol_type="genomic DNA"
           /db_xref="taxon:4529"
           /clone="OR_BBa0055D11"
           /tissue_type="young leaves"
           /lab_host="DH10B-T1 phage resistant"
           /clone_lib="OR_BBa"
           /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      5.1%; Score 91; DB 9; Length 703;
Best Local Similarity 87.0%; Pred. No. 9.7e-12;
Matches 100; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAAATAATTCCTTATATATATGGGAC 60
Db 657 ACTTTGGATAATAAGTAAGTCACAGAAAAATAAATAATTCCTTATATATATGGGAC 598

QY 61 AGACGAGTGGTCAACAGTACAACTCAAAATTCCTTATATATATGGGAC 115
Db 597 AGACGAATGTTAAACAGTGCAGTAATAAACTCAAAATTCCTTATATATAGAAC 543

RESULT 11
CL788096/c
LOCUS      CL788096
DEFINITION OR_BB0106H03.f OR_BBa Oryza rufipogon genomic clone OR_BB0106H03
5', genomic survey sequence.
ACCESSION  CL788096
VERSION     CL788096.1 GI:50867747
KEYWORDS   GSS.
SOURCE     Oryza rufipogon
   ORGANISM Oryza rufipogon
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
           1 (bases 1 to 582)
           Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
           Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
           OMAP Project
           Unpublished (2004)
           Contact: Rod A. Wing
           Arizona Genomics Institute
           University of Arizona
           Forbes Building Room 303, Tucson, AZ 85721-0036, USA
           Tel: 520 626 9595
           Fax: 520 621 1259
           Email: http://genome.arizona.edu
           PCR Primers
           FORWARD: TAA TAC GAC TCA CTA TAG GG
           BACKWARD: CAC TCA TTA GGC ACC CCA
           Insert Length: 161 Std Error: 0.00
           Plate: 0106 row: H column: 03
           Seq primer: TAA TAC GAC TCA CTA TAG GG
           Class: BAC ends.

TITLE      OMAP Project
JOURNAL    Unpublished (2004)
COMMENT    Contact: Rod A. Wing
           Arizona Genomics Institute
           University of Arizona
           Forbes Building Room 303, Tucson, AZ 85721-0036, USA
           Tel: 520 626 9595
           Fax: 520 621 1259
           Email: http://genome.arizona.edu
           PCR Primers
           FORWARD: TAA TAC GAC TCA CTA TAG GG
           BACKWARD: CAC TCA TTA GGC ACC CCA
           Plate: 0046 row: L column: 09
           Seq primer: CAC TCA TTA GGC ACC CCA
           Class: BAC ends.

FEATURES   Location/Qualifiers
   source  1..660
           /organism="Oryza rufipogon"
           /mol_type="genomic DNA"
           /db_xref="taxon:4529"
           /clone="OR_CBa0046L09"
           /tissue_type="young leaves"
           /dev_stage="2 week old seedlings"
           /lab_host="DH10B T1 phage resistant"
           /clone_lib="OR_CBa"
           /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
           drk treated 36 hrs before harvest"

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FEATURES   Location/Qualifiers
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           /organism="Oryza rufipogon"
           /mol_type="genomic DNA"
           /db_xref="taxon:4529"
           /clone="OR_BB0106H03"
           /tissue_type="young leaves"
           /lab_host="DH10B-T1 phage resistant"
           /clone_lib="OR_BBa"
           /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      5.1%; Score 90.4; DB 9; Length 582;
Best Local Similarity 75.7%; Pred. No. 1.3e-11;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAAAAATAAATAATTCCTTATATATGGGACTTATA 60
Db 315 ACTGTGGATAATAAGTAAGTCACAAATAAATAAATAAATTTTAAATTTTGAATA 256

QY 61 AGACGAGTGGTCAACAGTACAACTCAAAATTCCTTATATATGGGACTTATA 120
Db 255 AGACGAGTGGTCAACAGTGTGAACAAAATACTTAAATCTCTTATATTCGGGCGGATG 196

QY 121 TTATGGGACGGAGAGTAGAAGATTGT 148
Db 195 GAGTGCTAGTGTAGTAGTAGTAGTGTGT 168

RESULT 12
CL826141/c
LOCUS      CL826141
DEFINITION OR_CBa0046L09.r OR_CBa Oryza rufipogon genomic clone OR_CBa0046L09
3', genomic survey sequence.
ACCESSION  CL826141
VERSION     CL826141.1 GI:51071751
KEYWORDS   GSS.
SOURCE     Oryza rufipogon
   ORGANISM Oryza rufipogon
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
           1 (bases 1 to 660)
           Kim,H., Yu,Y., Wisotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
           Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
           Wing,R.
           OMAP Project
           Unpublished (2004)
           Contact: Rod A. Wing
           Arizona Genomics Institute
           University of Arizona
           Forbes Building Room 303, Tucson, AZ 85721-0036, USA
           Tel: 520 626 9595
           Fax: 520 621 1259
           Email: http://genome.arizona.edu
           PCR Primers
           FORWARD: TAA TAC GAC TCA CTA TAG GG
           BACKWARD: CAC TCA TTA GGC ACC CCA
           Plate: 0046 row: L column: 09
           Seq primer: CAC TCA TTA GGC ACC CCA
           Class: BAC ends.

FEATURES   Location/Qualifiers
   source  1..660
           /organism="Oryza rufipogon"
           /mol_type="genomic DNA"
           /db_xref="taxon:4529"
           /clone="OR_CBa0046L09"
           /tissue_type="young leaves"
           /dev_stage="2 week old seedlings"
           /lab_host="DH10B T1 phage resistant"
           /clone_lib="OR_CBa"
           /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
           drk treated 36 hrs before harvest"

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ORIGIN

Query Match 5.1%; Score 90.4; DB 9; Length 660;
 Best Local Similarity 75.7%; Pred. No. 1.4e-11;
 Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTACAGTCAAGTAAAGTAAATCCAAATTTTAAATA 60
 |||||
 Db 329 ACTGTGATAATAAGTACAGTCAAGTAAATCCAAATTTTAAATA 270
 |||||

QY 61 AGACGAGTGTCAACAGTCAAGTAAAGTAAATCCAAATTTTAAATA 120
 |||||
 Db 269 AGATGAGTGTCAACAGTGTGTAAGCAAAACTTAAATCTCTTATATCTCGGCGGATG 210
 |||||

QY 121 TTATGGGCGGAGGAGTGAAGATGT 148
 |||||
 Db 209 GAGTGTAGTGTAGTAGTAGTAGTGT 182
 |||||

RESULT 13
 CL795980/c
 LOCUS
 DEFINITION OR_CBA0005P13.f OR CBA Oryza rufipogon genomic clone OR_CBA0005P13
 5', genomic survey sequence.
 ACCESSION
 VERSION CL795980
 KEYWORDS
 SOURCE GSS
 ORGANISM Oryza rufipogon

REFERENCE
 AUTHORS Kim,H., Yu,Y., Wiesotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu

PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0005 row: P column: 13
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

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 source
 Location/Qualifiers
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 /clone="OR_CBA0005P13"
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 /lab_host="DH10B T1 phage resistant"
 /clone_lib="OR_CBA"
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 drk treated 36 hrs before harvest"

ORIGIN

Query Match 5.1%; Score 90.2; DB 9; Length 764;
 Best Local Similarity 92.2%; Pred. No. 1.6e-11;
 Matches 106; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 ACTTTAGATAATAAGTACAGTCAAGTAAATCCAAATTTTAAATA 60
 |||||
 Db 415 ACTTTGGATAATAAGTAAATCCACAA-AAAAATAATAATATCTCTAAATTTTAAATA 357
 |||||

QY 61 AGACGAGTGTCAACAGTCAAGTAAAGTAAATCCAAATTTTAAATA 115
 |||||
 Db 356 AGACGAGTGTCAACAGTCAAGTAAATCCAAATTTTAAATA 302
 |||||

RESULT 14
 CL732636
 LOCUS
 DEFINITION OR_BB00065D13.f OR BBA Oryza rufipogon genomic clone OR_BB00065D13
 5', genomic survey sequence.
 ACCESSION
 VERSION CL732636
 KEYWORDS
 SOURCE GSS
 ORGANISM Oryza rufipogon

REFERENCE
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu

PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0065 row: D column: 13
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES
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 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BB00065D13"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /clone_lib="OR_BBA"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 5.0%; Score 89.4; DB 9; Length 881;
 Best Local Similarity 86.1%; Pred. No. 2.5e-11;
 Matches 99; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTACAGTCAAGTAAATCCAAATTTTAAATA 60
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 Db 614 ACTGTAGATAATAAGTGTAGTACACAAATAAAATAATAATTTTAAATA 673
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QY 61 AGACGAGTGTCAACAGTCAAGTAAAGTAAATCCAAATTTTAAATA 115
 |||||
 Db 674 AGACGAGTGTCAACAGTGTACAGCAAAACTTAAATCCCTTATATATGGGAC 728
 |||||

RESULT 15
 CL617540/c
 LOCUS
 DEFINITION OR_BB00010K04.r OR BBA Oryza rufipogon genomic clone OR_BB00010K04
 3', Genomic survey sequence.
 ACCESSION
 VERSION CL617540
 KEYWORDS
 SOURCE GSS
 ORGANISM Oryza rufipogon

REFERENCE
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu

PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0005 row: P column: 13
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..881
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BB00010K04"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /clone_lib="OR_BBA"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 566)
Kim.H., Yu.Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

OMAP Project
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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Plate: 0010 row: K column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .566
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa0010K04"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR BBa"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

FEATURES
source

ORIGIN

Query Match 5.0%; Score 88; DB 9; Length 566;
Best Local Similarity 90.5%; Pred. No. 5.4e-11;
Matches 105; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ACTTTAGATATAAGTAAGTCACAGAAATAAATAAATCCAAA-TTTTTTTAAT 59
Db 530 ACTTTGGATATAAAGTAAGTCACAGAAATAAATAAATCCAAA-TTTTTTTAAT 471
Qy 60 AAGACGAGTGGTCAACAGTACAAAGTAAAACTCAAAATTCCTTATATTATGGGAC 115
Db 470 AAGACGATGGTCAACAGTCAAGCAAAACTCAAAATCCCTTATATTATGGGAC 415

Search completed: November 17, 2004, 14:35:00
Job time : 5098 secs